

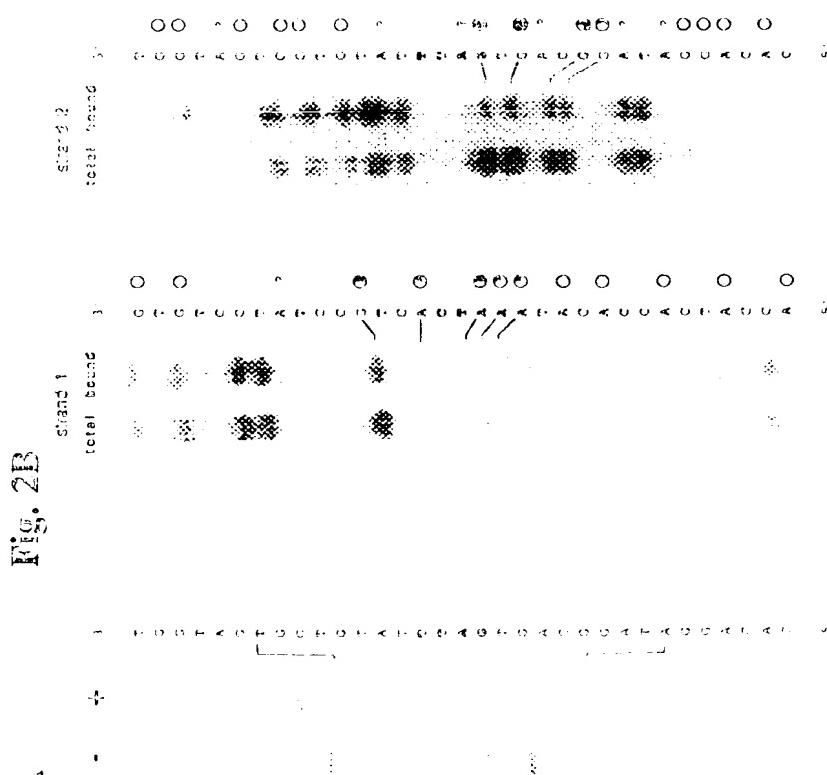
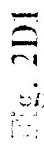
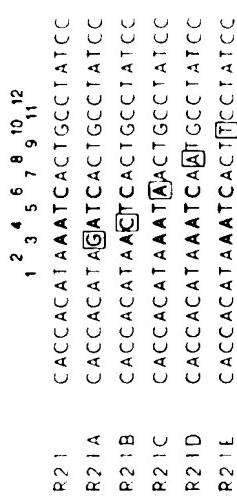
Fig. 1

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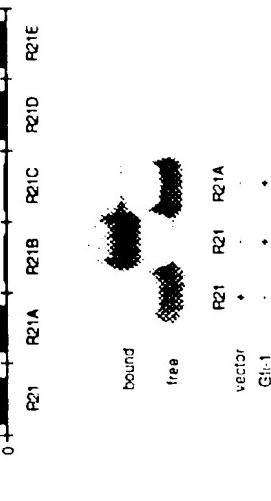
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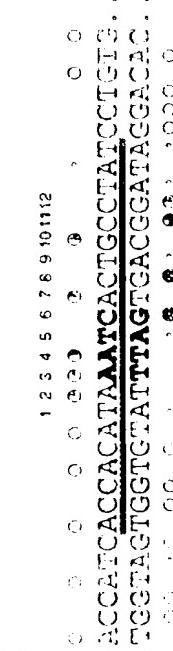
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Fig. 3A HCMV MIE Promoter

GCCCGCTGCTGAAACGGCCCAACTGGGACTTTCCATTGACGTCAATG
ACGTATGTTCCATAGTAACGCCAATAGGGACTTTCCATTGACGTCAATG
GGTGGAGTAACTTACCGTAAACTGCCCACTTGGCAGTACATCAAGTGATTC
ATATGCCAAAGTACGCCCTTATGACGTCAATGACGGTAAATGCCCGCC
TGGCATATTGCCAGTACATGACCTTATGGGACTTTCTACTTGGCAGTA
CATCTACGTATTAGTCATCGCTATTACCATGGTATGGTATGGGTTTGGCAGT
ACATCAATGGGGTGGATAGCGGGTTGACTGACGGGGATTTGCAAGTC

Fig. 3C Point Mutations

	Gli-1 site #1	Gli-1 site #2
Wildtype CMV	CACGGG <u>GAA</u> TTTCAAA <u>AATCA</u> ACGGG
Mutant A	CACGGG <u>GAT</u> TTTCAAA <u>GTC</u> AAACGGG
Mutant B	CACGGG <u>GAC</u> TTTCAAA <u>ACT</u> AAACGGG

Fig. 3D

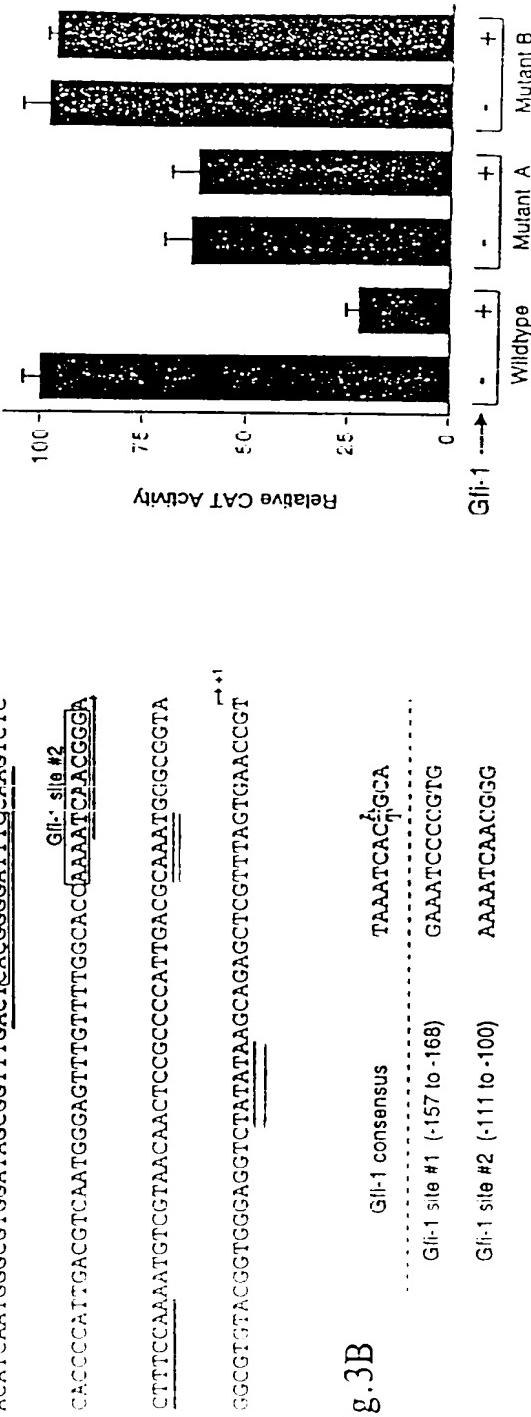


Fig. 3B

Gli-1 consensus TAAATCACGCA
Gli-1 site #1 (-157 to -168) GAAATCCCCGTC
Gli-1 site #2 (-111 to -100) AAAATCAACGGG

Fig. 4A

GII-1	Predicted	Binding Site		R21
		3'	5'	
finger 1	T	G	V	H
finger 2	S	O	R	T
finger 3	T	O	D	K
finger 4	N	T	R	D
finger 5	-	C	R	R
finger 6	G/I	C	G/I	G/I

Fig. 4B